

SEQUENCE LISTING

<110> Haseltine et al.

<120> Human DNA Mismatch Repair Proteins

<130> PF106P3D1

<140> Not assigned

<141> 2002-02-22

<150> PCT/US95/01035

<151> 1995-01-25

<150> 08/468,024

<151> 1995-06-06

<150> 08/465,769

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<150> 08/294,312

<151> 1994-08-23

<150> 08/210,143

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<170> PatentIn version 3.0

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Asn Leu Asn Glu Asp Ser Cys Asn Lys Lys Ser Asn Val Ile Asp Asn	
540 545 550 555	
aaa tct gga aaa gtt aca gct tat gat tta ctt agc aat cga gta atc	1793
Lys Ser Gly Lys Val Thr Ala Tyr Asp Leu Leu Ser Asn Arg Val Ile	

560										565					570					
aag	aaa	ccc	atg	tca	gca	agt	gct	ctt	ttt	ggt	caa	gat	cat	cgt	cct	1841				
Lys	Lys	Pro	Met	Ser	Ala	Ser	Ala	Leu	Phe	Val	Gln	Asp	His	Arg	Pro					
575					580					585										
cag	ttt	ctc	ata	gaa	aat	cct	aag	act	agt	tta	gag	gat	gca	aca	cta	1889				
Gln	Phe	Leu	Ile	Glu	Asn	Pro	Lys	Thr	Ser	Leu	Glu	Asp	Ala	Thr	Leu					
590					595					600										
caa	att	gaa	gaa	ctg	tgg	aag	aca	ttg	agt	gaa	gag	gaa	aaa	ctg	aaa	1937				
Gln	Ile	Glu	Glu	Leu	Trp	Lys	Thr	Leu	Ser	Glu	Glu	Glu	Lys	Leu	Lys					
605					610					615										
tat	gaa	gag	aag	gct	act	aaa	gac	ttg	gaa	cga	tac	aat	agt	caa	atg	1985				
Tyr	Glu	Glu	Lys	Ala	Thr	Lys	Asp	Leu	Glu	Arg	Tyr	Asn	Ser	Gln	Met					
620					625					630					635					
aag	aga	gcc	att	gaa	cag	gag	tca	caa	atg	tca	cta	aaa	gat	ggc	aga	2033				
Lys	Arg	Ala	Ile	Glu	Gln	Glu	Ser	Gln	Met	Ser	Leu	Lys	Asp	Gly	Arg					
640					645					650										
aaa	aag	ata	aaa	ccc	acc	agc	gca	tgg	aat	ttg	gcc	cag	aag	cac	aag	2081				
Lys	Lys	Ile	Lys	Pro	Thr	Ser	Ala	Trp	Asn	Leu	Ala	Gln	Lys	His	Lys					
655					660					665										
tta	aaa	acc	tca	tta	tct	aat	caa	cca	aaa	ctt	gat	gaa	ctc	ctt	cag	2129				
Leu	Lys	Thr	Ser	Leu	Ser	Asn	Gln	Pro	Lys	Leu	Asp	Glu	Leu	Leu	Gln					
670					675					680										
tcc	caa	att	gaa	aaa	aga	agg	agt	caa	aat	att	aaa	atg	gta	cag	atc	2177				
Ser	Gln	Ile	Glu	Lys	Arg	Arg	Ser	Gln	Asn	Ile	Lys	Met	Val	Gln	Ile					
685					690					695										
ccc	ttt	tct	atg	aaa	aac	tta	aaa	ata	aat	ttt	aag	aaa	caa	aac	aaa	2225				
Pro	Phe	Ser	Met	Lys	Asn	Leu	Lys	Ile	Asn	Phe	Lys	Lys	Gln	Asn	Lys					
700					705					710					715					
ggt	gac	tta	gaa	gag	aag	gat	gaa	cct	tgc	ttg	atc	cac	aat	ctc	agg	2273				
Val	Asp	Leu	Glu	Glu	Lys	Asp	Glu	Pro	Cys	Leu	Ile	His	Asn	Leu	Arg					
720					725					730										
ttt	cct	gat	gca	tgg	cta	atg	aca	tcc	aaa	aca	gag	gta	atg	tta	tta	2321				
Phe	Pro	Asp	Ala	Trp	Leu	Met	Thr	Ser	Lys	Thr	Glu	Val	Met	Leu	Leu					
735					740					745										
aat	cca	tat	aga	gta	gaa	gaa	gcc	ctg	cta	ttt	aaa	aga	ctt	ctt	gag	2369				
Asn	Pro	Tyr	Arg	Val	Glu	Glu	Ala	Leu	Leu	Phe	Lys	Arg	Leu	Leu	Glu					
750					755					760										
aat	cat	aaa	ctt	cct	gca	gag	cca	ctg	gaa	aag	cca	att	atg	tta	aca	2417				
Asn	His	Lys	Leu	Pro	Ala	Glu	Pro	Leu	Glu	Lys	Pro	Ile	Met	Leu	Thr					
765					770					775										
gag	agt	ctt	ttt	aat	gga	tct	cat	tat	tta	gac	gtt	tta	tat	aaa	atg	2465				
Glu	Ser	Leu	Phe	Asn	Gly	Ser	His	Tyr	Leu	Asp	Val	Leu	Tyr	Lys	Met					
780					785					790					795					
aca	gca	gat	gac	caa	aga	tac	agt	gga	tca	act	tac	ctg	tct	gat	cct	2513				
Thr	Ala	Asp	Asp	Gln	Arg	Tyr	Ser	Gly	Ser	Thr	Tyr	Leu	Ser	Asp	Pro					

800	805	810	
cgt ctt aca gcg aat ggt ttc aag ata aaa ttg ata cca gga gtt tca			2561
Arg Leu Thr Ala Asn Gly Phe Lys Ile Lys Leu Ile Pro Gly Val Ser			
815	820	825	
att act gaa aat tac ttg gaa ata gaa gga atg gct aat tgt ctc cca			2609
Ile Thr Glu Asn Tyr Leu Glu Ile Glu Gly Met Ala Asn Cys Leu Pro			
830	835	840	
ttc tat gga gta gca gat tta aaa gaa att ctt aat gct ata tta aac			2657
Phe Tyr Gly Val Ala Asp Leu Lys Glu Ile Leu Asn Ala Ile Leu Asn			
845	850	855	
aga aat gca aag gaa gtt tat gaa tgt aga cct cgc aaa gtg ata agt			2705
Arg Asn Ala Lys Glu Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser			
860	865	870	875
tat tta gag gga gaa gca gtg cgt cta tcc aga caa tta ccc atg tac			2753
Tyr Leu Glu Gly Glu Ala Val Arg Leu Ser Arg Gln Leu Pro Met Tyr			
880	885	890	
tta tca aaa gag gac atc caa gac att atc tac aga atg aag cac cag			2801
Leu Ser Lys Glu Asp Ile Gln Asp Ile Ile Tyr Arg Met Lys His Gln			
895	900	905	
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Phe Gly Asn Glu Ile Lys Glu Cys Val His Gly Arg Pro Phe Phe His			
910	915	920	
cat tta acc tat ctt cca gaa act aca tga ttaaatatgt ttaagaagat			2899
His Leu Thr Tyr Leu Pro Glu Thr Thr			
925	930		
tagttaccat tgaaattggt tctgtcataa aacagcatga gtctgggtttt aaattatctt			2959
tgtattatgt gtcacatggt tatttttttaa atgaggattc actgacttgt ttttatattg			3019
aaaaaagttc cacgtattgt agaaaacgta aataaactaa taac			3063

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Leu Asp Ala Gly Ala Thr Ser Val Asp Val Lys Leu Glu Asn Tyr Gly
 35 40 45

Phe Asp Lys Ile Glu Val Arg Asp Asn Gly Glu Gly Ile Lys Ala Val
50 55 60

Asp Ala Pro Val Met Ala Met Lys Tyr Tyr Thr Ser Lys Ile Asn Ser
65 70 75 80

His Glu Asp Leu Glu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala
85 90 95

Leu Gly Ser Ile Cys Cys Ile Ala Glu Val Leu Ile Thr Thr Arg Thr
100 105 110

Ala Ala Asp Asn Phe Ser Thr Gln Tyr Val Leu Asp Gly Ser Gly His
115 120 125

Ile Leu Ser Gln Lys Pro Ser His Leu Gly Gln Gly Thr Thr Val Thr
130 135 140

Ala Leu Arg Leu Phe Lys Asn Leu Pro Val Arg Lys Gln Phe Tyr Ser
145 150 155 160

Thr Ala Lys Lys Cys Lys Asp Glu Ile Lys Lys Ile Gln Asp Leu Leu
165 170 175

Met Ser Phe Gly Ile Leu Lys Pro Asp Leu Arg Ile Val Phe Val His
180 185 190

Asn Lys Ala Val Ile Trp Gln Lys Ser Arg Val Ser Asp His Lys Met
195 200 205

Ala Leu Met Ser Val Leu Gly Thr Ala Val Met Asn Asn Met Glu Ser
210 215 220

Phe Gln Tyr His Ser Glu Glu Ser Gln Ile Tyr Leu Ser Gly Phe Leu
225 230 235 240

Pro Lys Cys Asp Ala Asp His Ser Phe Thr Ser Leu Ser Thr Pro Glu
245 250 255

Arg Ser Phe Ile Phe Ile Asn Ser Arg Pro Val His Gln Lys Asp Ile
260 265 270

Leu Lys Leu Ile Arg His His Tyr Asn Leu Lys Cys Leu Lys Glu Ser
275 280 285

Thr Arg Leu Tyr Pro Val Phe Phe Leu Lys Ile Asp Val Pro Thr Ala
 290 295 300

Asp Val Asp Val Asn Leu Thr Pro Asp Lys Ser Gln Val Leu Leu Gln
 305 310 315 320

Asn Lys Glu Ser Val Leu Ile Ala Leu Glu Asn Leu Met Thr Thr Cys
 325 330 335

Tyr Gly Pro Leu Pro Ser Thr Asn Ser Tyr Glu Asn Asn Lys Thr Asp
 340 345 350

Val Ser Ala Ala Asp Ile Val Leu Ser Lys Thr Ala Glu Thr Asp Val
 355 360 365

Leu Phe Asn Lys Val Glu Ser Ser Gly Lys Asn Tyr Ser Asn Val Asp
 370 375 380

Thr Ser Val Ile Pro Phe Gln Asn Asp Met His Asn Asp Glu Ser Gly
 385 390 395 400

Lys Asn Thr Asp Asp Cys Leu Asn His Gln Ile Ser Ile Gly Asp Phe
 405 410 415

Gly Tyr Gly His Cys Ser Ser Glu Ile Ser Asn Ile Asp Lys Asn Thr
 420 425 430

Lys Asn Ala Phe Gln Asp Ile Ser Met Ser Asn Val Ser Trp Glu Asn
 435 440 445

Ser Gln Thr Glu Tyr Ser Lys Thr Cys Phe Ile Ser Ser Val Lys His
 450 455 460

Thr Gln Ser Glu Asn Gly Asn Lys Asp His Ile Asp Glu Ser Gly Glu
 465 470 475 480

Asn Glu Glu Glu Ala Gly Leu Glu Asn Ser Ser Glu Ile Ser Ala Asp
 485 490 495

Glu Trp Ser Arg Gly Asn Ile Leu Lys Asn Ser Val Gly Glu Asn Ile
 500 505 510

Glu Pro Val Lys Ile Leu Val Pro Glu Lys Ser Leu Pro Cys Lys Val
 515 520 525

Ser Asn Asn Asn Tyr Pro Ile Pro Glu Gln Met Asn Leu Asn Glu Asp
530 535 540

Ser Cys Asn Lys Lys Ser Asn Val Ile Asp Asn Lys Ser Gly Lys Val
545 550 555 560

Thr Ala Tyr Asp Leu Leu Ser Asn Arg Val Ile Lys Lys Pro Met Ser
565 570 575

Ala Ser Ala Leu Phe Val Gln Asp His Arg Pro Gln Phe Leu Ile Glu
580 585 590

Asn Pro Lys Thr Ser Leu Glu Asp Ala Thr Leu Gln Ile Glu Glu Leu
595 600 605

Trp Lys Thr Leu Ser Glu Glu Glu Lys Leu Lys Tyr Glu Glu Lys Ala
610 615 620

Thr Lys Asp Leu Glu Arg Tyr Asn Ser Gln Met Lys Arg Ala Ile Glu
625 630 635 640

Gln Glu Ser Gln Met Ser Leu Lys Asp Gly Arg Lys Lys Ile Lys Pro
645 650 655

Thr Ser Ala Trp Asn Leu Ala Gln Lys His Lys Leu Lys Thr Ser Leu
660 665 670

Ser Asn Gln Pro Lys Leu Asp Glu Leu Leu Gln Ser Gln Ile Glu Lys
675 680 685

Arg Arg Ser Gln Asn Ile Lys Met Val Gln Ile Pro Phe Ser Met Lys
690 695 700

Asn Leu Lys Ile Asn Phe Lys Lys Gln Asn Lys Val Asp Leu Glu Glu
705 710 715 720

Lys Asp Glu Pro Cys Leu Ile His Asn Leu Arg Phe Pro Asp Ala Trp
725 730 735

Leu Met Thr Ser Lys Thr Glu Val Met Leu Leu Asn Pro Tyr Arg Val
740 745 750

Glu Glu Ala Leu Leu Phe Lys Arg Leu Leu Glu Asn His Lys Leu Pro
755 760 765

Ala Glu Pro Leu Glu Lys Pro Ile Met Leu Thr Glu Ser Leu Phe Asn
770 775 780

Gly Ser His Tyr Leu Asp Val Leu Tyr Lys Met Thr Ala Asp Asp Gln
785 790 795 800

Arg Tyr Ser Gly Ser Thr Tyr Leu Ser Asp Pro Arg Leu Thr Ala Asn
805 810 815

Gly Phe Lys Ile Lys Leu Ile Pro Gly Val Ser Ile Thr Glu Asn Tyr
820 825 830

Leu Glu Ile Glu Gly Met Ala Asn Cys Leu Pro Phe Tyr Gly Val Ala
835 840 845

Asp Leu Lys Glu Ile Leu Asn Ala Ile Leu Asn Arg Asn Ala Lys Glu
850 855 860

Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser Tyr Leu Glu Gly Glu
865 870 875 880

Ala Val Arg Leu Ser Arg Gln Leu Pro Met Tyr Leu Ser Lys Glu Asp
885 890 895

Ile Gln Asp Ile Ile Tyr Arg Met Lys His Gln Phe Gly Asn Glu Ile
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Lys Glu Cys Val His Gly Arg Pro Phe Phe His His Leu Thr Tyr Leu
915 920 925

Pro Glu Thr Thr
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1 5

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Glu Pro Ala Lys Ala Ile Lys Pro Ile Asp Arg Lys Ser Val His Gln

10	15	20	25	
att tgc tct ggg cag gtg gta ctg agt cta agc act gcg gta aag gag				147
Ile Cys Ser Gly	Gln Val Val Leu Ser	Leu Ser Thr Ala Val Lys Glu		
	30	35	40	
tta gta gaa aac agt ctg gat gct ggt gcc act aat att gat cta aag				195
Leu Val Glu Asn Ser Leu Asp Ala Gly Ala Thr Asn Ile Asp Leu Lys				
	45	50	55	
ctt aag gac tat gga gtg gat ctt att gaa gtt tca gac aat gga tgt				243
Leu Lys Asp Tyr Gly Val Asp Leu Ile Glu Val Ser Asp Asn Gly Cys				
	60	65	70	
ggg gta gaa gaa gaa aac ttc gaa ggc tta act ctg aaa cat cac aca				291
Gly Val Glu Glu Glu Asn Phe Glu Gly Leu Thr Leu Lys His His Thr				
	75	80	85	
tct aag att caa gag ttt gcc gac cta act cag gtt gaa act ttt ggc				339
Ser Lys Ile Gln Glu Phe Ala Asp Leu Thr Gln Val Glu Thr Phe Gly				
	90	95	100	105
ttt cgg ggg gaa gct ctg agc tca ctt tgt gca ctg agc gat gtc acc				387
Phe Arg Gly Glu Ala Leu Ser Ser Leu Cys Ala Leu Ser Asp Val Thr				
	110	115	120	
att tct acc tgc cac gca tcg gcg aag gtt gga act cga ctg atg ttt				435
Ile Ser Thr Cys His Ala Ser Ala Lys Val Gly Thr Arg Leu Met Phe				
	125	130	135	
gat cac aat ggg aaa att atc cag aaa acc ccc tac ccc cgc ccc aga				483
Asp His Asn Gly Lys Ile Ile Gln Lys Thr Pro Tyr Pro Arg Pro Arg				
	140	145	150	
ggg acc aca gtc agc gtg cag cag tta ttt tcc aca cta cct gtg cgc				531
Gly Thr Thr Val Ser Val Gln Gln Leu Phe Ser Thr Leu Pro Val Arg				
	155	160	165	
cat aag gaa ttt caa agg aat att aag aag gag tat gcc aaa atg gtc				579
His Lys Glu Phe Gln Arg Asn Ile Lys Lys Glu Tyr Ala Lys Met Val				
	170	175	180	185
cag gtc tta cat gca tac tgt atc att tca gca ggc atc cgt gta agt				627
Gln Val Leu His Ala Tyr Cys Ile Ile Ser Ala Gly Ile Arg Val Ser				
	190	195	200	
tgc acc aat cag ctt gga caa gga aaa cga cag cct gtg gta tgc aca				675
Cys Thr Asn Gln Leu Gly Gln Gly Lys Arg Gln Pro Val Val Cys Thr				
	205	210	215	
ggt gga agc ccc agc ata aag gaa aat atc ggc tct gtg ttt ggg cag				723
Gly Gly Ser Pro Ser Ile Lys Glu Asn Ile Gly Ser Val Phe Gly Gln				
	220	225	230	
aag cag ttg caa agc ctc att cct ttt gtt cag ctg ccc cct agt gac				771
Lys Gln Leu Gln Ser Leu Ile Pro Phe Val Gln Leu Pro Pro Ser Asp				
	235	240	245	
tcc gtg tgt gaa gag tac ggt ttg agc tgt tcg gat gct ctg cat aat				819
Ser Val Cys Glu Glu Tyr Gly Leu Ser Cys Ser Asp Ala Leu His Asn				

250	255	260	265	
ctt ttt tac atc tca ggt ttc att tca caa tgc acg cat gga gtt gga Leu Phe Tyr Ile Ser Gly Phe Ile Ser Gln Cys Thr His Gly Val Gly	270	275	280	867
agg agt tca aca gac aga cag ttt ttc ttt atc aac cgg cgg cct tgt Arg Ser Ser Thr Asp Arg Gln Phe Phe Phe Ile Asn Arg Arg Pro Cys	285	290	295	915
gac cca gca aag gtc tgc aga ctc gtg aat gag gtc tac cac atg tat Asp Pro Ala Lys Val Cys Arg Leu Val Asn Glu Val Tyr His Met Tyr	300	305	310	963
aat cga cac cag tat cca ttt gtt gtt ctt aac att tct gtt gat tca Asn Arg His Gln Tyr Pro Phe Val Val Leu Asn Ile Ser Val Asp Ser	315	320	325	1011
gaa tgc gtt gat atc aat gtt act cca gat aaa agg caa att ttg cta Glu Cys Val Asp Ile Asn Val Thr Pro Asp Lys Arg Gln Ile Leu Leu	330	335	340	1059
caa gag gaa aag ctt ttg ttg gca gtt tta aag acc tct ttg ata gga Gln Glu Glu Lys Leu Leu Leu Ala Val Leu Lys Thr Ser Leu Ile Gly	350	355	360	1107
atg ttt gat agt gat gtc aac aag cta aat gtc agt cag cag cca ctg Met Phe Asp Ser Asp Val Asn Lys Leu Asn Val Ser Gln Gln Pro Leu	365	370	375	1155
ctg gat gtt gaa ggt aac tta ata aaa atg cat gca gcg gat ttg gaa Leu Asp Val Glu Gly Asn Leu Ile Lys Met His Ala Ala Asp Leu Glu	380	385	390	1203
aag ccc atg gta gaa aag cag gat caa tcc cct tca tta agg act gga Lys Pro Met Val Glu Lys Gln Asp Gln Ser Pro Ser Leu Arg Thr Gly	395	400	405	1251
gaa gaa aaa aaa gac gtg tcc att tcc aga ctg cga gag gcc ttt tct Glu Glu Lys Lys Asp Val Ser Ile Ser Arg Leu Arg Glu Ala Phe Ser	410	415	420	1299
ctt cgt cac aca aca gag aac aag cct cac agc cca aag act cca gaa Leu Arg His Thr Thr Glu Asn Lys Pro His Ser Pro Lys Thr Pro Glu	430	435	440	1347
cca aga agg agc cct cta gga cag aaa agg ggt atg ctg tct tct agc Pro Arg Arg Ser Pro Leu Gly Gln Lys Arg Gly Met Leu Ser Ser Ser	445	450	455	1395
act tca ggt gcc atc tct gac aaa ggc gtc ctg aga cct cag aaa gag Thr Ser Gly Ala Ile Ser Asp Lys Gly Val Leu Arg Pro Gln Lys Glu	460	465	470	1443
gca gtg agt tcc agt cac gga ccc agt gac cct acg gac aga gcg gag Ala Val Ser Ser Ser His Gly Pro Ser Asp Pro Thr Asp Arg Ala Glu	475	480	485	1491
gtg gag aag gac tcg ggg cac ggc agc act tcc gtg gat tct gag ggg Val Glu Lys Asp Ser Gly His Gly Ser Thr Ser Val Asp Ser Glu Gly				1539

490	495	500	505	
ttc agc atc cca gac acg ggc agt cac tgc agc agc gag tat gcg gcc				1587
Phe Ser Ile Pro Asp Thr Gly Ser His Cys Ser Ser Glu Tyr Ala Ala	510	515	520	
agc tcc cca ggg gac agg ggc tgc cag gaa cat gtg gac tct cag gag				1635
Ser Ser Pro Gly Asp Arg Gly Ser Gln Glu His Val Asp Ser Gln Glu	525	530	535	
aaa gcg cct gaa act gac gac tct ttt tca gat gtg gac tgc cat tca				1683
Lys Ala Pro Glu Thr Asp Asp Ser Phe Ser Asp Val Asp Cys His Ser	540	545	550	
aac cag gaa gat acc gga tgt aaa ttt cga gtt ttg cct cag cca act				1731
Asn Gln Glu Asp Thr Gly Cys Lys Phe Arg Val Leu Pro Gln Pro Thr	555	560	565	
aat ctc gca acc cca aac aca aag cgt ttt aaa aaa gaa gaa att ctt				1779
Asn Leu Ala Thr Pro Asn Thr Lys Arg Phe Lys Lys Glu Glu Ile Leu	570	575	580	585
tcc agt tct gac att tgt caa aag tta gta aat act cag gac atg tca				1827
Ser Ser Ser Asp Ile Cys Gln Lys Leu Val Asn Thr Gln Asp Met Ser	590	595	600	
gcc tct cag gtt gat gta gct gtg aaa att aat aag aaa gtt gtg ccc				1875
Ala Ser Gln Val Asp Val Ala Val Lys Ile Asn Lys Lys Val Val Pro	605	610	615	
ctg gac ttt tct atg agt tct tta gct aaa cga ata aag cag tta cat				1923
Leu Asp Phe Ser Met Ser Ser Leu Ala Lys Arg Ile Lys Gln Leu His	620	625	630	
cat gaa gca cag caa agt gaa ggg gaa cag aat tac agg aag ttt agg				1971
His Glu Ala Gln Gln Ser Glu Gly Glu Gln Asn Tyr Arg Lys Phe Arg	635	640	645	
gca aag att tgt cct gga gaa aat caa gca gcc gaa gat gaa cta aga				2019
Ala Lys Ile Cys Pro Gly Glu Asn Gln Ala Ala Glu Asp Glu Leu Arg	650	655	660	665
aaa gag ata agt aaa acg atg ttt gca gaa atg gaa atc att ggt cag				2067
Lys Glu Ile Ser Lys Thr Met Phe Ala Glu Met Glu Ile Ile Gly Gln	670	675	680	
ttt aac ctg gga ttt ata ata acc aaa ctg aat gag gat atc ttc ata				2115
Phe Asn Leu Gly Phe Ile Ile Thr Lys Leu Asn Glu Asp Ile Phe Ile	685	690	695	
gtg gac cag cat gcc acg gac gag aag tat aac ttc gag atg ctg cag				2163
Val Asp Gln His Ala Thr Asp Glu Lys Tyr Asn Phe Glu Met Leu Gln	700	705	710	
cag cac acc gtg ctc cag ggg cag agg ctc ata gca cct cag act ctc				2211
Gln His Thr Val Leu Gln Gly Gln Arg Leu Ile Ala Pro Gln Thr Leu	715	720	725	
aac tta act gct gtt aat gaa gct gtt ctg ata gaa aat ctg gaa ata				2259
Asn Leu Thr Ala Val Asn Glu Ala Val Leu Ile Glu Asn Leu Glu Ile				

730	735	740	745	
ttt aga aag aat ggc ttt gat ttt gtt atc gat gaa aat gct cca gtc				2307
Phe Arg Lys Asn Gly Phe Asp Phe Val Ile Asp Glu Asn Ala Pro Val				
750		755	760	
act gaa agg gct aaa ctg att tcc ttg cca act agt aaa aac tgg acc				2355
Thr Glu Arg Ala Lys Leu Ile Ser Leu Pro Thr Ser Lys Asn Trp Thr				
765		770	775	
ttc gga ccc cag gac gtc gat gaa ctg atc ttc atg ctg agc gac agc				2403
Phe Gly Pro Gln Asp Val Asp Glu Leu Ile Phe Met Leu Ser Asp Ser				
780		785	790	
cct ggg gtc atg tgc cgg cct tcc cga gtc aag cag atg ttt gcc tcc				2451
Pro Gly Val Met Cys Arg Pro Ser Arg Val Lys Gln Met Phe Ala Ser				
795		800	805	
aga gcc tgc cgg aag tcg gtg atg att ggg act gct ctt aac aca agc				2499
Arg Ala Cys Arg Lys Ser Val Met Ile Gly Thr Ala Leu Asn Thr Ser				
810		815	820	825
gag atg aag aaa ctg atc acc cac atg ggg gag atg gac cac ccc tgg				2547
Glu Met Lys Lys Leu Ile Thr His Met Gly Glu Met Asp His Pro Trp				
830		835	840	
aac tgt ccc cat gga agg cca acc atg aga cac atc gcc aac ctg ggt				2595
Asn Cys Pro His Gly Arg Pro Thr Met Arg His Ile Ala Asn Leu Gly				
845		850	855	
gtc att tct cag aac tga ccgtagtcac tgtatggaat aattggtttt				2643
Val Ile Ser Gln Asn				
860				
atcgcagatt tttatgtttt gaaagacaga gtcttcacta accttttttg ttttaaaatg				2703
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ttcaaacc				2771

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Pro	Ile	Asp	Arg	Lys	Ser	Val	His	Gln	Ile	Cys	Ser	Gly	Gln	Val	Val
			20					25					30		

Leu	Ser	Leu	Ser	Thr	Ala	Val	Lys	Glu	Leu	Val	Glu	Asn	Ser	Leu	Asp
		35					40					45			

Ala Gly Ala Thr Asn Ile Asp Leu Lys Leu Lys Asp Tyr Gly Val Asp
50 55 60

Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe
65 70 75 80

Glu Gly Leu Thr Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala
85 90 95

Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser
100 105 110

Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Ala Ser
115 120 125

Ala Lys Val Gly Thr Arg Leu Met Phe Asp His Asn Gly Lys Ile Ile
130 135 140

Gln Lys Thr Pro Tyr Pro Arg Pro Arg Gly Thr Thr Val Ser Val Gln
145 150 155 160

Gln Leu Phe Ser Thr Leu Pro Val Arg His Lys Glu Phe Gln Arg Asn
165 170 175

Ile Lys Lys Glu Tyr Ala Lys Met Val Gln Val Leu His Ala Tyr Cys
180 185 190

Ile Ile Ser Ala Gly Ile Arg Val Ser Cys Thr Asn Gln Leu Gly Gln
195 200 205

Gly Lys Arg Gln Pro Val Val Cys Thr Gly Gly Ser Pro Ser Ile Lys
210 215 220

Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile
225 230 235 240

Pro Phe Val Gln Leu Pro Pro Ser Asp Ser Val Cys Glu Glu Tyr Gly
245 250 255

Leu Ser Cys Ser Asp Ala Leu His Asn Leu Phe Tyr Ile Ser Gly Phe
260 265 270

Ile Ser Gln Cys Thr His Gly Val Gly Arg Ser Ser Thr Asp Arg Gln
275 280 285

Phe Phe Phe Ile Asn Arg Arg Pro Cys Asp Pro Ala Lys Val Cys Arg
 290 295 300

Leu Val Asn Glu Val Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe
 305 310 315 320

Val Val Leu Asn Ile Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val
 325 330 335

Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu
 340 345 350

Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Val Asn
 355 360 365

Lys Leu Asn Val Ser Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu
 370 375 380

Ile Lys Met His Ala Ala Asp Leu Glu Lys Pro Met Val Glu Lys Gln
 385 390 395 400

Asp Gln Ser Pro Ser Leu Arg Thr Gly Glu Glu Lys Lys Asp Val Ser
 405 410 415

Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu Arg His Thr Thr Glu Asn
 420 425 430

Lys Pro His Ser Pro Lys Thr Pro Glu Pro Arg Arg Ser Pro Leu Gly
 435 440 445

Gln Lys Arg Gly Met Leu Ser Ser Ser Thr Ser Gly Ala Ile Ser Asp
 450 455 460

Lys Gly Val Leu Arg Pro Gln Lys Glu Ala Val Ser Ser Ser His Gly
 465 470 475 480

Pro Ser Asp Pro Thr Asp Arg Ala Glu Val Glu Lys Asp Ser Gly His
 485 490 495

Gly Ser Thr Ser Val Asp Ser Glu Gly Phe Ser Ile Pro Asp Thr Gly
 500 505 510

Ser His Cys Ser Ser Glu Tyr Ala Ala Ser Ser Pro Gly Asp Arg Gly
 515 520 525

Ser Gln Glu His Val Asp Ser Gln Glu Lys Ala Pro Glu Thr Asp Asp
 530 535 540

Ser Phe Ser Asp Val Asp Cys His Ser Asn Gln Glu Asp Thr Gly Cys
 545 550 555 560

Lys Phe Arg Val Leu Pro Gln Pro Thr Asn Leu Ala Thr Pro Asn Thr
 565 570 575

Lys Arg Phe Lys Lys Glu Glu Ile Leu Ser Ser Ser Asp Ile Cys Gln
 580 585 590

Lys Leu Val Asn Thr Gln Asp Met Ser Ala Ser Gln Val Asp Val Ala
 595 600 605

Val Lys Ile Asn Lys Lys Val Val Pro Leu Asp Phe Ser Met Ser Ser
 610 615 620

Leu Ala Lys Arg Ile Lys Gln Leu His His Glu Ala Gln Gln Ser Glu
 625 630 635 640

Gly Glu Gln Asn Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu
 645 650 655

Asn Gln Ala Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Thr Met
 660 665 670

Phe Ala Glu Met Glu Ile Ile Gly Gln Phe Asn Leu Gly Phe Ile Ile
 675 680 685

Thr Lys Leu Asn Glu Asp Ile Phe Ile Val Asp Gln His Ala Thr Asp
 690 695 700

Glu Lys Tyr Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Gly
 705 710 715 720

Gln Arg Leu Ile Ala Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu
 725 730 735

Ala Val Leu Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp
 740 745 750

Phe Val Ile Asp Glu Asn Ala Pro Val Thr Glu Arg Ala Lys Leu Ile
 755 760 765

Ser Leu Pro Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Val Asp
 770 775 780

Glu Leu Ile Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro
 785 790 795 800

Ser Arg Val Lys Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val
 805 810 815

Met Ile Gly Thr Ala Leu Asn Thr Ser Glu Met Lys Lys Leu Ile Thr
 820 825 830

His Met Gly Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro
 835 840 845

Thr Met Arg His Ile Ala Asn Leu Gly Val Ile Ser Gln Asn
 850 855 860

<210> 7
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hMLH1 sense primer

<400> 7
 gttgaacatc tagacgtctc

20

<210> 8
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hMLH1 sense primer

<400> 8
 tcgtggcagg gggtattcg

19

<210> 9
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hMLH1 sense primer

<400> 9
 ctaccaatg cctcaaccg

19

<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 sense primer

<400> 10
gagaactgat agaaattgga tg

22

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 sense primer

<400> 11
gggacatgag gttctccg

18

<210> 12
<211> 19
<212> DNA
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<220>
<223> hMLH1 sense primer

<400> 12
gggctgtgtg aatcctcag

19

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 antisense primer

<400> 13
cggttcacca ctgtctcgtc

20

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 antisense primer

<400> 14
tccaggatgc tctcctcg

18

<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 antisense primer

<400> 15
caagtcctgg tagcaaagtc

20

<210> 16
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 antisense primer

<400> 16
atggcaaggt caaagagcg

19

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 antisense primer

<220>
<221> misc_feature
<222> (22)..(22)
<223> n equals a, t, g or c

<400> 17
caacaatgta ttcagnaagt cc

22

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH1 antisense primer

<400> 18
ttgatacaac actttgtatc g

21

<210> 19
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> hMLH1 antisense primer

<400> 19

ggaatactat cagaaggcaa g

21

<210> 20

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 sense primer

<400> 20

acagagcaag ttactcagat g

21

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 sense primer

<400> 21

gtacacaatg caggcattag

20

<210> 22

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 sense primer

<400> 22

aatgtggatg ttaatgtgca c

21

<210> 23

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 sense primer

<400> 23

ctgacctcgt cttcctac

18

<210> 24

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> hMLH1 sense primer
 <400> 24
 cagcaagatg aggagatgc 19

 <210> 25
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> hMLH1 sense primer

 <400> 25
 ggaaatggtg gaagatgatt c 21

 <210> 26
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> hMLH1 sense primer

 <400> 26
 cttctcaaca ccaagc 16

 <210> 27
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> hMLH1 sense primer

 <400> 27
 gaaattgatg aggaagggaa c 21

 <210> 28
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> hMLH1 sense primer

 <400> 28
 cttctgattg acaactatgt gc 22

 <210> 29
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> hMLH1 sense primer	
<400> 29	22
cacagaagat ggaaatatcc tg	
<210> 30	
<211> 20	
<212> DNA	
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<220>	
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<400> 30	20
gtggttgtag cacttaagac	
<210> 31	
<211> 20	
<212> DNA	
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<400> 31	20
tttcccatat tcttcacttg	
<210> 32	
<211> 19	
<212> DNA	
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<223> hMLH1 antisense primer	
<400> 32	19
gtaacatgag ccacatggc	
<210> 33	
<211> 19	
<212> DNA	
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<220>	
<223> hMLH1 antisense primer	
<400> 33	19
ccactgtctc gtccagccg	
<210> 34	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	

<223> hMLH1 5' primer with BamHI restriction site
 <400> 34
 cgggatccat gtcgttcgtg gcaggg 26

 <210> 35
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> hMLH1 3' primer with XbaI restriction site
 <400> 35
 gctctagatt aacacctctc aaagac 26

 <210> 36
 <211> 21
 <212> DNA
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 <220>
 <223> hMLH1 primer useful for amplifying codons 1 to 394
 <400> 36
 gcattctagac gtttccttgg c 21

 <210> 37
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer useful for amplifying codons 1 to 394 of hMLH1
 <400> 37
 catccaagct tctgttcccg 20

 <210> 38
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer useful for amplifying codons 326 to 729 of hMLH1
 <400> 38
 ggggtgcagc agcacatcg 19

 <210> 39
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> primer useful for amplifying codons 326 to 729 of hMLH1

<400> 39
ggaggcagaa tgtgtgagcg 20

<210> 40
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 602 to 756 plus 128
nucleotides of 3' untranslated sequence of hMLH1

<400> 40
tcccaaagaa ggacttgct 19

<210> 41
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 602 to 756 plus 128
nucleotides of 3' untranslated sequence of hMLH1

<400> 41
agtataagtc ttaagtgcta cc 22

<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 578 to 632 of hMLH1

<400> 42
tttatggttt ctcacctgcc 20

<210> 43
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 578 to 632 of hMLH1

<400> 43
gttatctgcc cacctcagc 19

<210> 44
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
 <223> primer useful for amplifying codons 1 to 394 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 44
 ggatcctaatacgcactcactatagggagac caccatggca tctagacgtt tcccttggc 59

<210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer useful for amplifying codons 1 to 394 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 45
 catccaagct tctgttcccg 20

<210> 46
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer useful for amplifying codons 326 to 729 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 46
 ggatcctaatacgcactcactatagggagac caccatgggg gtgcagcagc acatcg 56

<210> 47
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer useful for amplifying codons 326 to 729 of hMLH1 wherein PCR product may be used for coupled transcription-translation

<400> 47
 ggaggcagaa tgtgtgagcg 20

<210> 48
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hMLH2 5' primer with a BamHI restriction site

<400> 48
 cgggatccat gaaacaattg cctgcggc 28

<210> 49
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> hMLH2 3' primer with XbaI restriction site

 <400> 49
 gctctagacc agactcatgc tgtttt 26

 <210> 50
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> hMLH3 5' primer with a BamHI restriction site

 <400> 50
 cgggatccat ggagcgagct gagagc 26

 <210> 51
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> hMLH3 3' primer with XbaI restriction site

 <400> 51
 gctctagagt gaagactctg tct 23

 <210> 52
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> hMLH2 primer

 <400> 52
 aagctgctct gttaaaagcg 20

 <210> 53
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> hMLH2 primer

 <400> 53
 gcaccagcat ccaaggag 18

<210> 54
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH3 primer

<400> 54
caaccatgag acacatcgc

19

<210> 55
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> hMLH3 primer

<400> 55
aggttagtga agactctgtc

20

<210> 56
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 1 to 500 of hMLH2

<400> 56
ggatcctaatac acgactcact atagggagac caccatggaa caattgcctg cgg

53

<210> 57
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 1 to 500 of hMLH2

<400> 57
cctgctccac tcactctgc

18

<210> 58
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 270 to 755 of hMLH2

<400> 58
ggatcctaatac acgactcact atagggagac caccatggaa gatattcttaa agttaatccg

60

<210> 59
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer useful for amplifying codons 270 to 755 of hMLH2

 <400> 59
 ggcttcttct actctatatg g 21

 <210> 60
 <211> 58
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer useful for amplifying from codon 485 to the translation
 termination site at codon 933 of hMLH2

 <400> 60
 ggatcctaatac gactcact ataggagac caccatggca ggtcttgaat actcttcg 58

 <210> 61
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer useful for amplifying from codon 485 to the translation
 termination site at codon 933 of hMLH2

 <400> 61
 aaaacaagtc agtgaatcct c 21

 <210> 62
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 3' primer useful for amplifying up to codon 369 of hMLH2

 <400> 62
 aagcacatct gtttctgctg 20

 <210> 63
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 3' primer useful for amplifying up to codon 290 of hMLH2

 <400> 63
 acgagtagat tcctttaggc 20

<210> 64
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 3' primer useful for amplifying up to codon 214 of hMLH2

 <400> 64
 cagaactgac atgagagcc 19

 <210> 65
 <211> 52
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer useful for amplifying codons 1 to 863 hMLH3

 <400> 65
 ggatcctaatac gactcact atagggagac caccatggag cgagctgaga gc 52

 <210> 66
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer useful for amplifying codons 1 to 863 hMLH3

 <400> 66
 aggttagtga agactctgtc 20

 <210> 67
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer useful for amplifying up to codon 472 of hMLH3

 <400> 67
 ctgaggtctc agcaggc 17

 <210> 68
 <211> 57
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer useful for amplifying codons 415 to 863 of hMLH3

 <400> 68
 ggatcctaatac gactcact atagggagac caccatgggtg tccatttcca gactgcg 57

<210> 69
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 415 to 863 of hMLH3

<400> 69
aggtttagtga agactctgtc 20

<210> 70
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 195 to 233 of hMLH2

<400> 70
ttatttggca gaaaagcaga g 21

<210> 71
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 195 to 233 of hMLH2

<400> 71
ttaaaagact aacctcttgc c 21

<210> 72
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> sequencing primer useful for sequencing codons 195 to 233 of hMLH2

<400> 72
ctgctgttat gaacaatatg g 21

<210> 73
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 233 to 257 of hMLH3

<400> 73

cagaagcagt tgcaaagcc
19

<210> 74
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 233 to 257 of hMLH3

<400> 74
aaaccgtact cttcacacac 20

<210> 75
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 347 of 377 of hMLH3

<400> 75
gaggaaaagc ttttgttggc 20

<210> 76
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 347 of 377 of hMLH3

<400> 76
cagtggctgc tgactgac 18

<210> 77
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 439 to 472 of hMLH3

<400> 77
tccagaacca agaaggagc 19

<210> 78
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> primer useful for amplifying codons 439 to 472 of hMLH3

